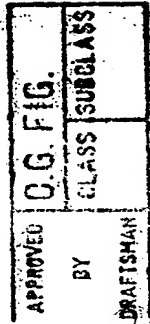




FIGURE 1A.1



ATG AAG CCG TAC TTC TGC CGT GTC TTT GTC TTC TGC TTC CTA ATC	45
M K P Y F C R V F V F C F L I	
5 10 15	
AGA CTT TTA ACA GGA GAA ATC AAT GGC TCG GCC GAT CAT AGG ATG	90
R L L T G *E I N G S A D H R M	
20 25 30	
TTT TCA TTT CAC AAT GGA GGT GTA CAG ATT TCT TGT AAA TAC CCT	135
F S F H N G G V Q I S C K Y P	
35 40 45	
GAG ACT GTC CAG CAG TTA AAA ATG CGA TTG TTC AGA GAG AGA GAA	180
E T V Q Q L K M R L F R E R E	
50 55 60	
GTC CTC TGC GAA CTC ACC AAG ACC AAG GGA AGC GGA AAT GCG GTG	225
V L C E L T K T K G S G N A V	
65 70 75	
TCC ATC AAG AAT CCA ATG CTC TGT CTA TAT CAT CTG TCA AAC AAC	270
S I K N P M L C L Y H L S N N	
80 85 90	
AGC GTC TCT TTT TTC CTA AAC AAC CCA GAC AGC TCC CAG GGA AGC	315
S V S F F L N N P D S S Q G S	
95 100 105	
TAT TAC TTC TGC AGC CTG TCC ATT TTT GAC CCA CCT CCT TTT CAA	360
Y Y F C S L S I F D P P P F Q	
110 115 120	
GAA AGG AAC CTT AGT GGA GGA TAT TTG CAT ATT TAT GAA TCC CAG	405
E R N L S G G Y L H I Y E S Q	
125 130 135	
CTC TGC TGC CAG CTG AAG CTC TGG CTA CCC GTA GGG TGT GCA GCT	450
L C C Q L K L W L P V G C A A	
140 145 150	
TTC GTT GTG GTA CTC CTT TTT GGA TGC ATA CTT ATC ATC TGG TTT	495
F V V V L L F G C I L I I W F	
155 160 165	
TCA AAA AAG AAA TAC GGA TCC AGT GTG CAT GAC CCT AAT AGT GAA	540
S K K K Y G S S V H D P N S E	
170 175 180	



FIGURE 1A.2

TAC	ATG	TTC	ATG	GCG	GCA	GTC	AAC	ACA	AAC	AAA	AAG	TCT	AGA	CTT	585
Y	M	F	M	A	A	V	N	T	N	K	K	S	R	L	
				185					190					195	
GCA GGT GTG ACC TCA															600
A	G	V	T	S											
				200											

APPROVED	O.G. FIG.	CLASS	SUBCLASS
BY			
DRAFTSMAN			



FIGURE 1B

mCRP1	MKPYFCRVFV	FCFLIRLL--	-----TGEIN	GS----	ADHR	MFSFHNGGVQ	39
mCD28	MT-----	----LRLFL	ALNFFSVQVT	ENKILVKQSP	LLVVDSNEVS		38
Consensus	M.....RLL..V.		
mCRP1	ISCKYPETV-	-QQLKMRLFR	--EREV-LCE	LTKTKGSGNA	VSIKNPMLCL		84
mCD28	LSCRYSYNLL	AKEFRASLYK	GVNSDVEVCV	GNGNFTYQPQ	FRSNAEFNCD		88
Consensus	.SC.Y.....L..V..C.C.		
mCRP1	YHLSNNSVSF	FLNPNDSQOG	SYFFCSLSIF	DPPPFQERNL	SGGYL-HIYE		133
mCD28	GDFDNETVTF	RLWNLHVNHT	DIYFCKIEFM	YPPPYLDNER	SNGTIIHIKE		138
ConsensusN..V..F	.L.N.....	..YFC.....	.PPP.....	S.G...HI.E		
mCRP1	SQLC---CQL	KL-W-LPVGC	AA-FVVVLLF	GCIL-IIWFS	KKKY----GS		172
mCD28	KHLCHTQSSP	KLFWALVVVA	GVLFCYGLLV	TVALCVIWTN	SRRNRLQVT		188
Consensus	..LC.....	KL.W.L.V..	...F...LL.	...L..IW..		
mCRP1	SVH-DPNSEY	MFMAAVNTNK	KSR-LAGVTS				200
mCD28	TMNMTPRRPG	LTRKPYQPYA	PARDFAAYRP				218
ConsensusP.....R..A....	...				

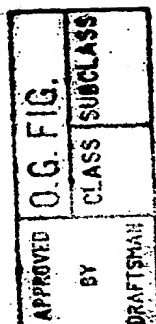




FIGURE 2A.1

ATG	CAG	CTA	AAG	TGT	CCC	TGT	TTT	GTG	TCC	TTG	GGA	ACC	AGG	CAG	45
M	Q	L	K	C	P	C	F	V	S	L	G	T	R	Q	
				5					10					15	
CCT	GTT	TGG	AAG	AAG	CTC	CAT	GTT	TCT	AGC	GGG	TTC	TTT	TCT	GGT	90
P	V	W	K	K	L	H	V	S	S	G	F	F	S	G	
				20					25					30	
CTT	GGT	CTG	TTC	TTG	CTG	CTG	TTG	AGC	AGC	CTC	TGT	GCT	GCC	TCT	135
L	G	L	F	L	L	L	L	S	S	L	C	A	A	S	
				35					40					45	
GCA	GAG	ACT	GAA	GTC	GGT	GCA	ATG	GTG	GGC	AGC	AAT	GTG	GTG	CTC	180
A	*E	T	E	V	G	A	M	V	G	S	N	V	V	L	
				50					55					60	
AGC	TGC	ATT	GAC	CCC	CAC	AGA	CGC	CAT	TTC	AAC	TTG	AGT	GGT	CTG	225
S	C	I	D	P	H	R	R	H	F	N	L	S	G	L	
				65					70					75	
TAT	GTC	TAT	TGG	CAA	ATC	GAA	AAC	CCA	GAA	GTT	TCG	GTG	ACT	TAC	270
Y	V	Y	W	Q	I	E	N	P	E	V	S	V	T	Y	
				80					85					90	
TAC	CTG	CCT	TAC	AAG	TCT	CCA	GGG	ATC	AAT	GTG	GAC	AGT	TCC	TAC	315
Y	L	P	Y	K	S	P	G	I	N	V	D	S	S	Y	
				95					100					105	
AAG	AAC	AGG	GGC	CAT	CTG	TCC	CTG	GAC	TCC	ATG	AAG	CAG	GGT	AAC	360
K	N	R	G	H	L	S	L	D	S	M	K	Q	G	N	
				110					115					120	
TTC	TCT	CTG	TAC	CTG	AAG	AAT	GTC	ACC	CCT	CAG	GAT	ACC	CAG	GAG	405
F	S	L	Y	L	K	N	V	T	P	Q	D	T	Q	E	
				125					130					135	
TTC	ACA	TGC	CGG	GTA	TTT	ATG	AAT	ACA	GCC	ACA	GAG	TTA	GTC	AAG	450
F	T	C	R	V	F	M	N	T	A	T	E	L	V	K	
				140					145					150	
ATC	TTG	GAA	GAG	GTG	GTC	AGG	CTG	CGT	GTG	GCA	GCA	AAC	TTC	AGT	495
I	L	E	E	V	V	R	L	R	V	A	A	N	F	S	
				155					160					165	
ACA	CCT	GTC	ATC	AGC	ACC	TCT	GAT	AGC	TCC	AAC	CCG	GGC	CAG	GAA	540
T	P	V	I	S	T	S	D	S	S	N	P	G	Q	E	
				170					175					180	

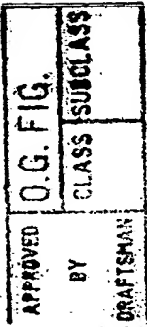




FIGURE 2A.2

CGT ACC TAC ACC TGC ATG TCC AAG AAT GGC TAC CCA GAG CCC AAC	585
R T Y T C M S K N G Y P E P N	
185 190 195	
CTG TAT TGG ATC AAC ACA ACG GAC AAT AGC CTA ATA GAC ACG GCT	630
L Y W I N T T D N S L I D T A	
200 205 210	
CTG CAG AAT AAC ACT GTC TAC TTG AAC AAG TTG GGC CTG TAT GAT	675
L Q N N T V Y L N K L G L Y D	
215 220 225	
GTA ATC AGC ACA TTA AGG CTC CCT TGG ACA TCT CGT GGG GAT GTT	720
V I S T L R L P W T S R G D V	
230 235 240	
CTG TGC TGC GTA GAG AAT GTG GCT CTC CAC CAG AAC ATC ACT AGC	765
L C C V E N V A L H Q N I T S	
245 250 255	
ATT AGC CAG GCA GAA AGT TTC ACT GGA AAT AAC ACA AAG AAC CCA	810
I S Q A E S F T G N N T K N P	
260 265 270	
CAG GAA ACC CAC AAT AAT GAG TTA AAA GTC CTT GTC CCC GTC CTT	855
Q E T H N N E L K V L V P V L	
275 280 285	
GCT GTA CTG GCG GCA GCG GCA TTC GTT TCC TTC ATC ATA TAC AGA	900
A V L A A A A F V S F I I Y R	
290 295 300	
CGC ACG CGT CCC CAC CGA AGC TAT ACA GGA CCC AAG ACT GTA CAG	945
R T R P H R S Y T G P K T V Q	
305 310 315	
CTT GAA CTT ACA GAC CAC GCC	966
L E L T D H A	
320 322	

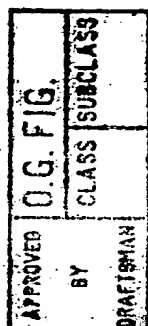




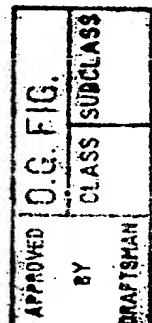
FIGURE 2B

APPROVED	BY	O.G. FIG.	
		CLASS	SUBCLASS
		CRAFTSMAN	

mB7RP1	MQLKPCPCFVS	LGTRQPVWKK	LHVSSGFFSG	LGLFLLLLS-	SLCAASAETE	49
mCD80	MA--CNC--Q	LMQDTPL---	LKFPCCPRI-	L-LFVLLIRL	SQVSSDVDEQ	41
Consensus	M...C.C...	L....P....	L.....	L.LF.LL...	S.....	
mB7RP1	VGAMVGSNVV	LSCIDPHRRH	FNLSGLYVYW	QIENPEVSVT	YYLPYKSPGI	99
mCD80	LSKSVKDKVL	LPC-RYNsph	EDESEDRIYW	QKHDKVV---	--LSVIAGKL	85
ConsensusV...V.	L.C.....	H...S....Y	WQ.....V...	..L.....	
mB7RP1	NVDSSYKNRG	HLSLDSMKQG	NFSLYLKNVT	PQDTQEFTCR	VFMNTATELV	149
mCD80	KVWPEYKNR-	--TL--YDNT	TYSLIILGLV	LSDRGTYSKV	VQKKERGTYE	130
Consensus	.V...YKNR.	...L.....	..SL.....	..D.....C.	V.....	
mB7RP1	KILEEVVRLR	VAANFSTPVI	STSDSSNPGQ	ERTYTCMSKN	GYPEPNLYWI	199
mCD80	VKHLALVKLS	IKADFSTPNI	TESGNPSADT	KRI-TCFASG	GFPKPRFSWL	179
ConsensusV.L.	..A.FSTP.I	..S.....	.R..TC....	G.P.P...W.	
mB7RP1	-NTTDNSLID	TALQNTVYL	NKLGLYDVIS	TLRLPWTSRG	DVLCCVENVA	248
mCD80	ENGRELPGIN	TTISQDPESE	LYTISSQLDF	NTTRNHTIKC	LIKYGDAHVS	229
Consensus	.N.....I.	T.....T...V.	
mB7RP1	LHQNITSISQ	AESFTGNNTK	NPQETHNNEL	KVLVPVLAVL	A-AAAFVSFI	297
mCD80	EDFTWEKPPE	DPPDSKNTLV	LFGAGFGAVI	TVVVIVVVIK	CFCKHRSCFR	279
ConsensusN...V.V.V....F.	
mB7RP1	IYRRTR-PHR	SYT-GPKTVQ	LELTDHA			322
mCD80	RNEASRETN	SLTFGPPEAL	AEQTVFL			306
ConsensusR....	S.T.GP....	.E.T...			



FIGURE 3A.1



ATG CGG CTG GGC AGT CCT GGA CTG CTC TTC CTG CTC TTC AGC AGC	45
M R L G S P G L L F L L F S S	
5 10 15	
CTT CGA GCT GAT ACT CAG GAG AAG GAA GTC AGA GCG ATG GTA GGC	90
L R A *D *T *Q *E K *E V R A *M V G	
20 25 30	
AGC GAC GTG GAG CTC AGC TGC GCT TGC CCT GAA GGA AGC CGT TTT	135
S D V E L S C A C P E G S R F	
35 40 45	
GAT TTA AAT GAT GTT TAC GTA TAT TGG CAA ACC AGT GAG TCG AAA	180
D L N D V Y V Y W Q T S E S K	
50 55 60	
ACC GTG GTG ACC TAC CAC ATC CCA CAG AAC AGC TCC TTG GAA AAC	225
T V V T Y H I P Q N S S L E N	
65 70 75	
GTG GAC AGC CGC TAC CGG AAC CGA GCC CTG ATG TCA CCG GCC GGC	270
V D S R Y R N R A L M S P A G	
80 85 90	
ATG CTG CGG GGC GAC TTC TCC CTG CGC TTG TTC AAC GTC ACC CCC	315
M L R G D F S L R L F N V T P	
95 100 105	
CAG GAC GAG CAG AAG TTT CAC TGC CTG GTG TTG AGC CAA TCC CTG	360
Q D E Q K F H C L V L S Q S L	
110 115 120	
GGA TTC CAG GAG GTT TTG AGC GTT GAG GTT ACA CTG CAT GTG GCA	405
G F Q E V L S V E V T L H V A	
125 130 135	
GCA AAC TTC AGC GTG CCC GTC GTC AGC GCC CCC CAC AGC CCC TCC	450
A N F S V P V V S A P H S P S	
140 145 150	
CAG GAT GAG CTC ACC TTC ACG TGT ACA TCC ATA AAC GGC TAC CCC	495
Q D E L T F T C T S I N G Y P	
155 160 165	
AGG CCC AAC GTG TAC TGG ATC AAT AAG ACG GAC AAC AGC CTG CTG	540
R P N V Y W I N K T D N S L L	
170 175 180	



FIGURE 3A.2

GAC CAG GCT CTG CAG AAT GAC ACC GTC TTC TTG AAC ATG CGG GGC	585
D Q A L Q N D T V F L N M R G	
185 190 195	
TTG TAT GAC GTG GTC AGC GTG CTG AGG ATC GCA CGG ACC CCC AGC	630
L Y D V V S V L R I A R T P S	
200 205 210	
GTG AAC ATT GGC TGC TGC ATA GAG AAC GTG CTT CTG CAG CAG AAC	675
V N I G C C I E N V L L Q Q N	
215 220 225	
CTG ACT GTC GGC AGC CAG ACA GGA AAT GAC ATC GGA GAG AGA GAC	720
L T V G S Q T G N D I G E R D	
230 235 240	
AAG ATC ACA GAG AAT CCA GTC AGT ACC GGC GAG AAA AAC GCG GCC	765
K I T E N P V S T G E K N A A	
245 250 255	
ACG TGG AGC ATC CTG GCT GTC CTG TGC CTG CTT GTG GTC GTG GCG	810
T W S I L A V L C L L V V V A	
260 265 270	
GTG GCC ATA GGC TGG GTG TGC AGG GAC CGA TGC CTC CAA CAC AGC	855
V A I G W V C R D R C L Q H S	
275 280 285	
TAT GCA GGT	864
Y A G	
288	

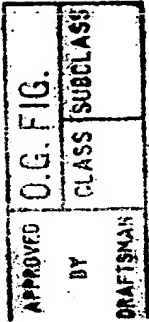
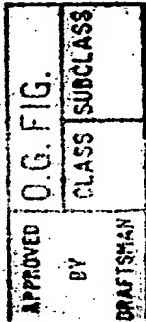




FIGURE 3B

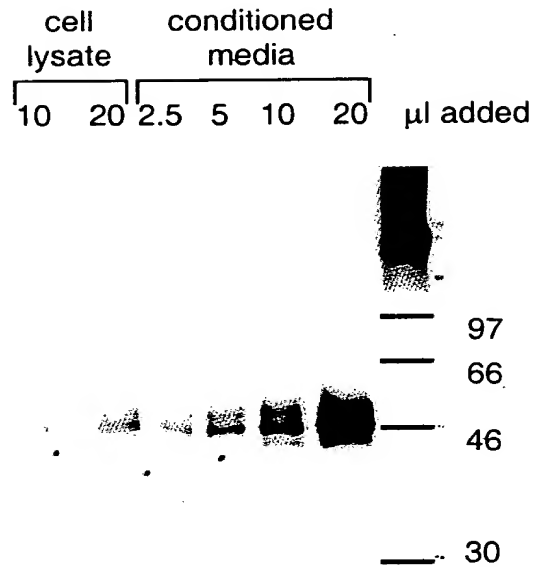
hB7RP1	EKEVRAMVGS	DVELSCACPE	GSRFDLNDVY	VYWQTSESKT	VVTYHIPQNS	50
mB7RP1	ETEVGAMVGS	NVLSCIDPH	RRHFNLSGLY	VYWQIENPEV	SVTYLTPYKS	50
Consensus	E.EV.AMVGS	.V.LSC..P.	...F.L...Y	VYWQ.....	.VTY..P..S	
hB7RP1	SLENVDSRYR	NRALMSPAGM	LRGDFSLRLF	NVTPQDEQKF	HCLVLSQ-SL	99
mB7RP1	PGINVDSYK	NRGHLSLDSM	KQGNFSLYLK	NVTPQDTQEF	TCRVFMNTAT	100
Consensus	...NVDS.Y.	NR...S...M	..G.FSL.L.	NVTPQD.Q.F	.C.V.....	
hB7RP1	GFQEVLSVEV	TLHVAANFSV	PVVSAPHSPS	Q-DELTFTCT	SINGYPRPNV	148
mB7RP1	ELVKILEEVV	RLRVAANFST	PVISTSDSSN	PGQERTYTCM	SKNGYPEPNL	150
ConsensusL...V	.L.VAANFS.	PV.S...S..	...E.T.TC.	S.NGY.P.N.	
hB7RP1	YWINKTDNSL	LDQALQNDTV	FLNMRGLYDV	VSVLRIARTP	SVNIGCCCIEN	198
mB7RP1	YWINTTDNSL	IDTALQNNVT	YLNKLGLYDV	ISTLRPPTS	RGDVLCCVEN	200
Consensus	YWIN.TDNSL	.D.ALQN.TV	.LN..GLYDV	.S.LR...T.CC.EN	
hB7RP1	VLLQQNLTVG	SQTGNDIGER	DKITENPVST	GEKNAATWSI	LAVLCLLVVV	248
mB7RP1	VALHQNITSI	SQAESFTGNN	TKNPQETHNN	ELKVLV--PV	LAVLAAAFV	248
Consensus	V.L.QN.T..	SQ.....G..	.K.....	..K.....	LAVL.....V	
hB7RP1	AVAIGWVCRD	RCLQHSYAG				267
mB7RP1	SFIIYR--RT	R-PHRSYTG	KTVQLELTDH	A		276
Consensus	...I....R.	R....SY.G.			





APPROVED	O.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

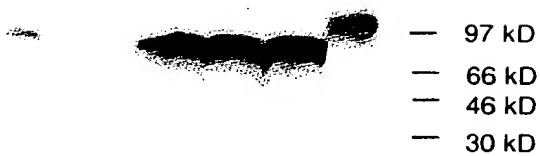
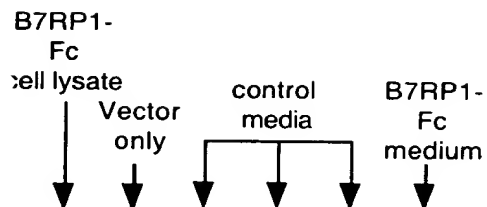
FIG. 4A





APPROVED	O.G. FIG.		CLASS	SUBCLASS
BY	DRAFTSMAN			

FIG. 4B





APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

FIG. 5

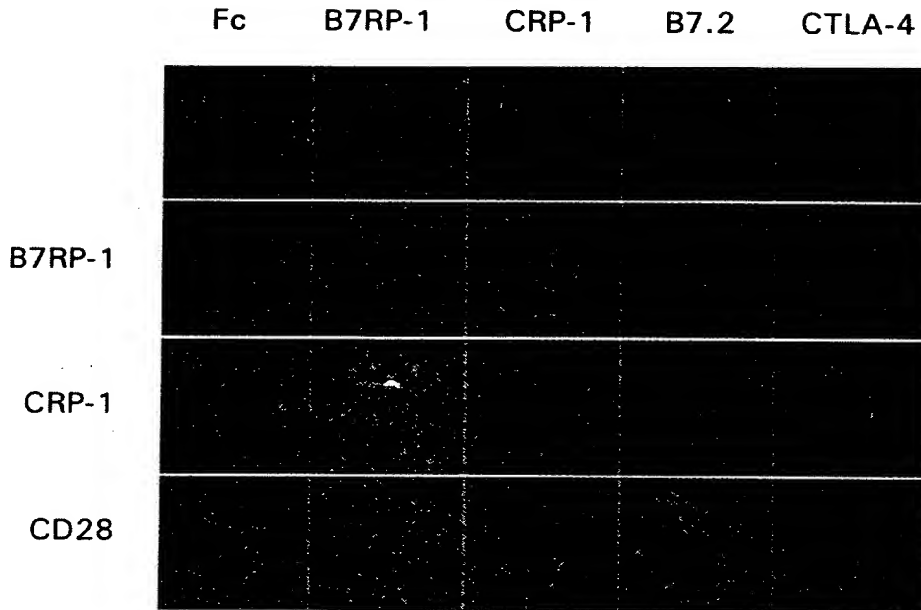




FIG. 6A

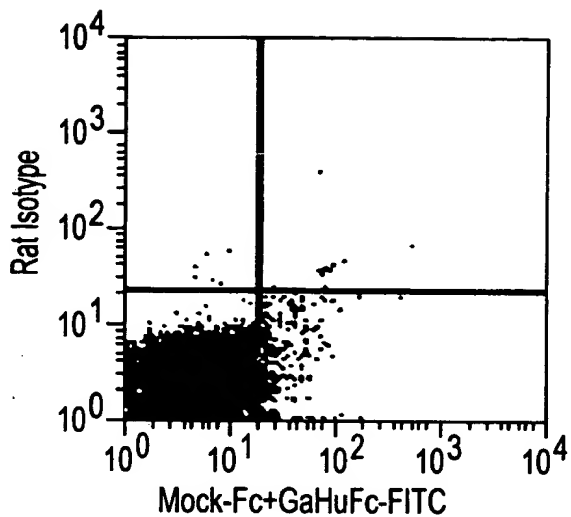


FIG. 6B

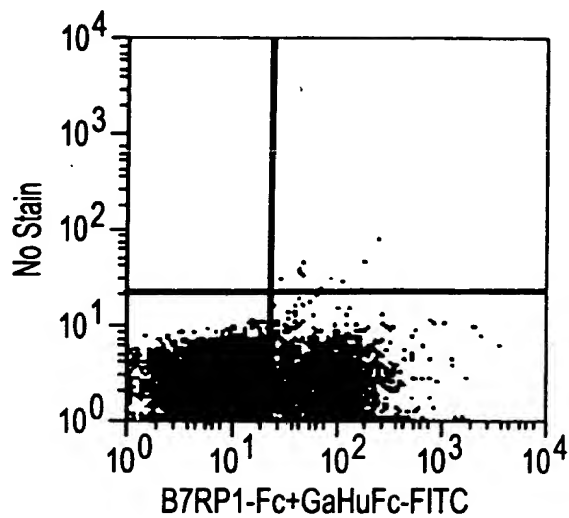


FIG. 6C

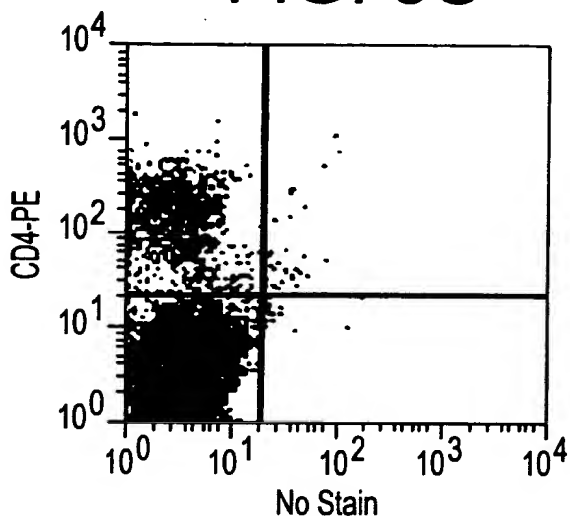


FIG. 6D

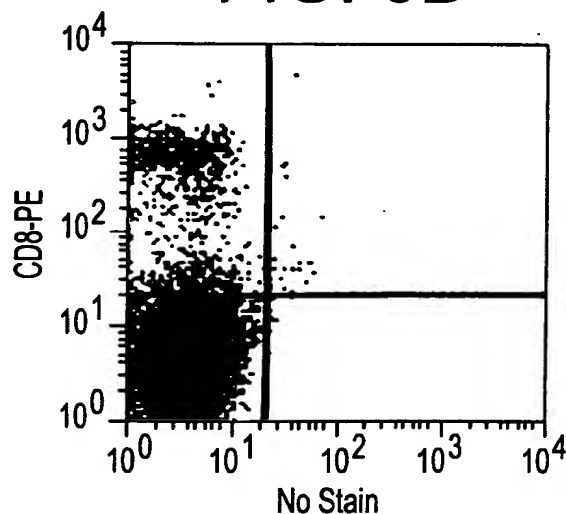


FIG. 6E

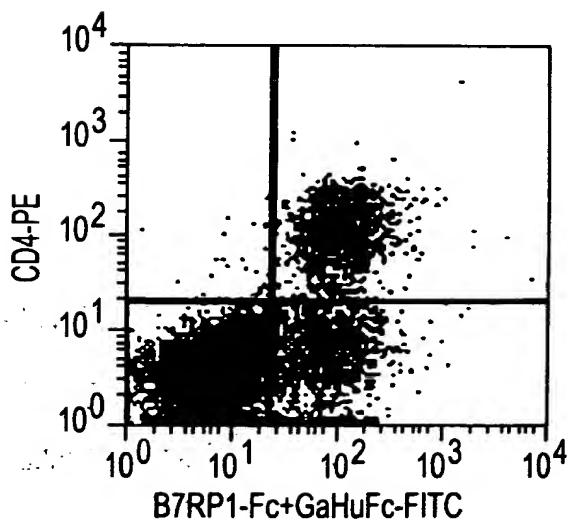
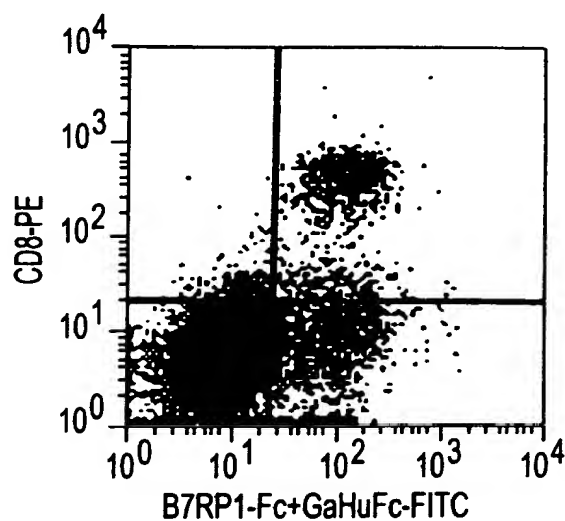


FIG. 6F



O.G. FIG.	
APPROVED	BY CLASS SUBCLASS
DRAFTSMAN	



O.G. FIG.	
APPROVED	BY
CLASS SUBCLASS	
DRAFTSMAN	

FIG. 7A

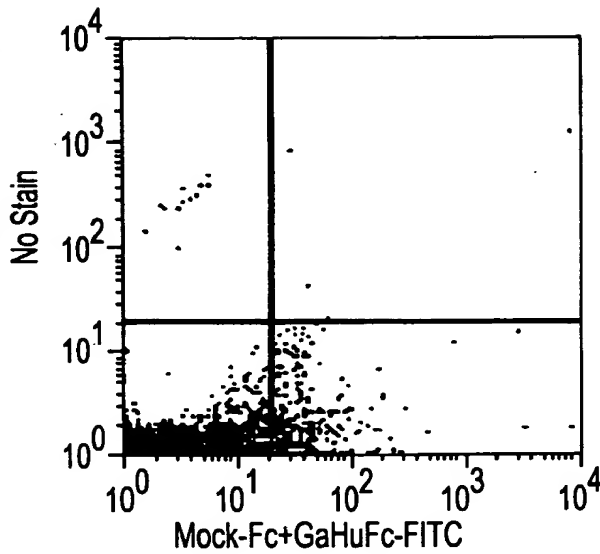


FIG. 7B

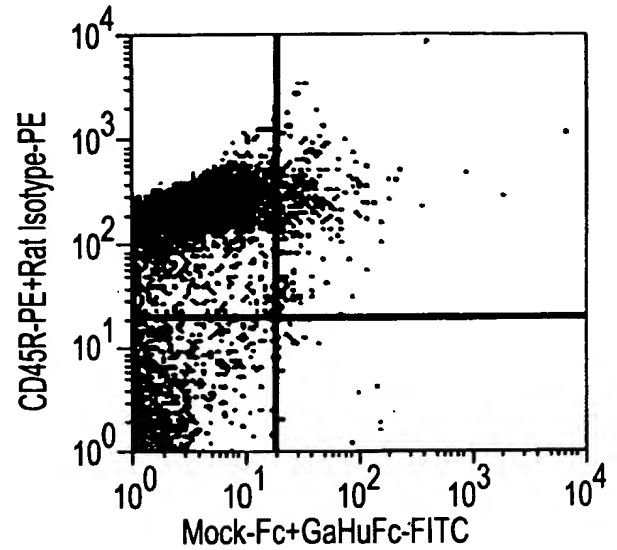
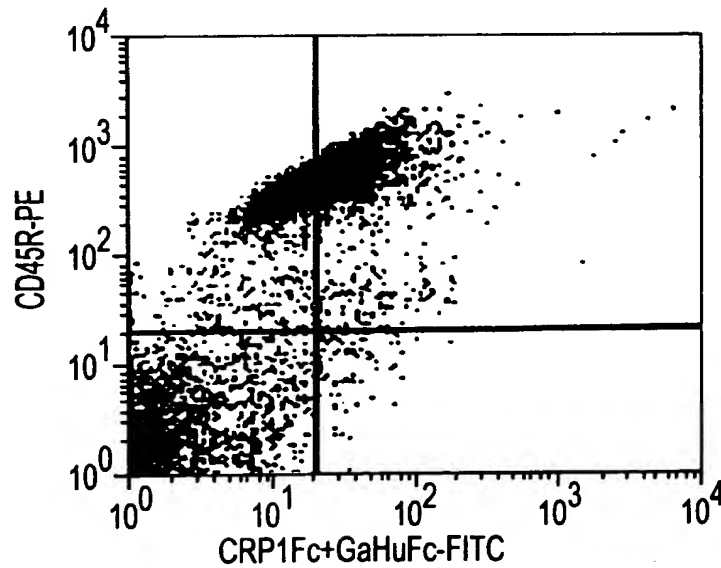


FIG. 7C





O.G. FIG.	
APPROVED	BY CLASS SUBCLASS
DRAFTSMAN	

FIG. 8A

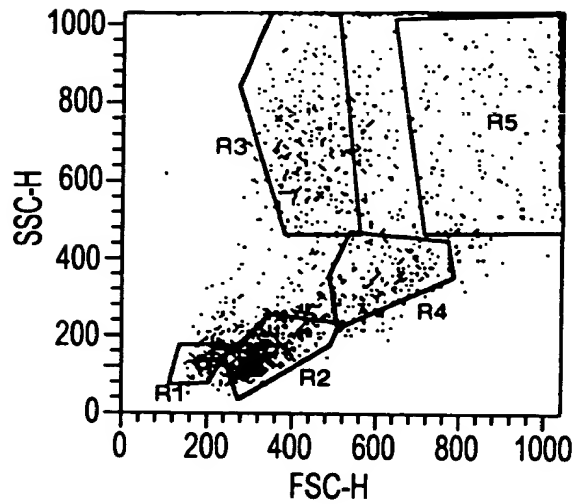


FIG. 8B

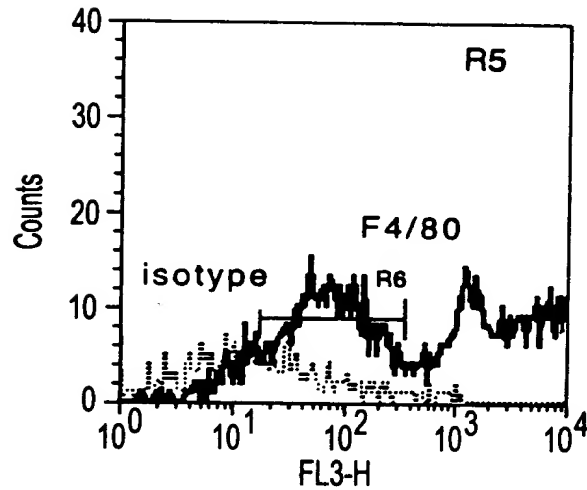
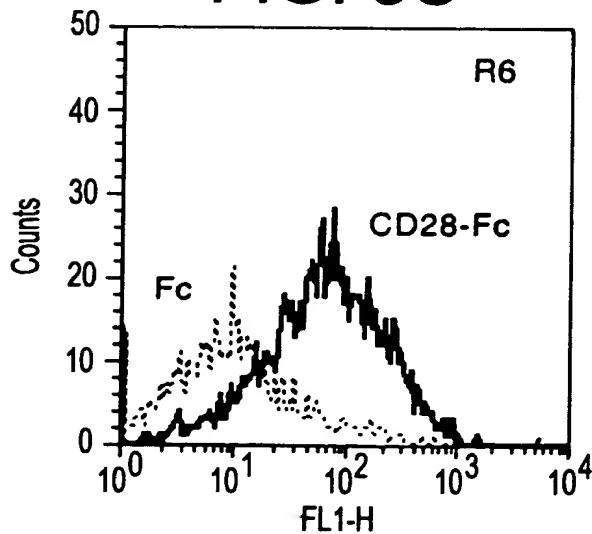


FIG. 8C





APPROVED	BY	CLASS	SUBCLASS
O.G. FIG.			
CRAFTSMAN			

FIG. 9

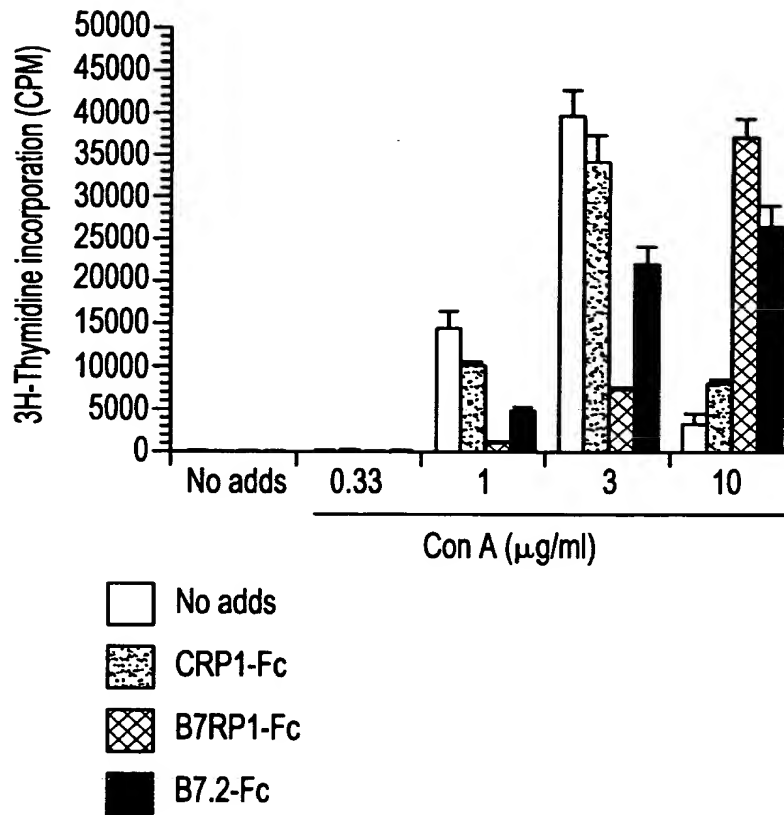




FIG. 10A

Lymph node-control#10

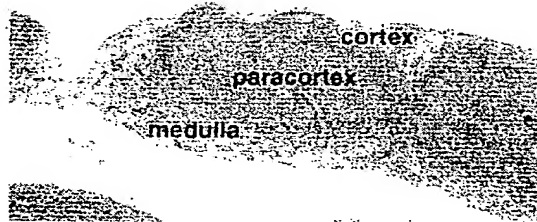


FIG. 10B

LN-WX11#40

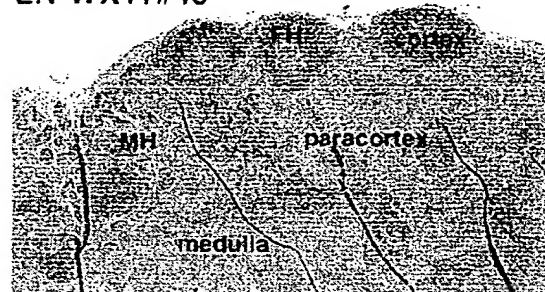


FIG. 10C

LN closeup-control#10

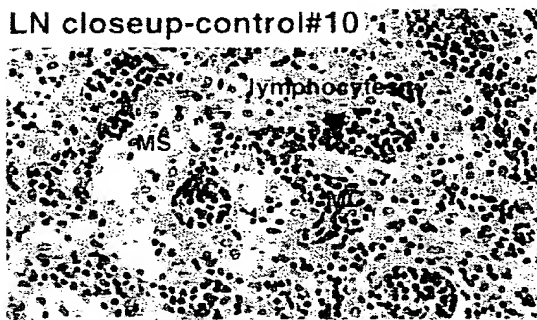


FIG. 10D

LN closeup-WX11#40

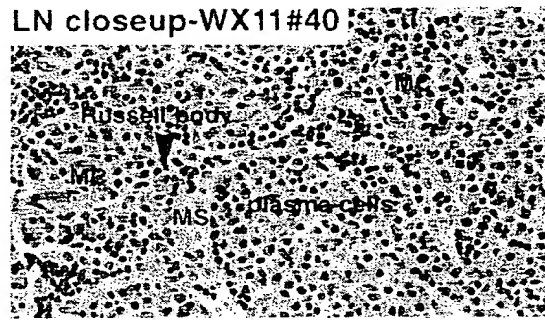


FIG. 10E

Spleen-control#10

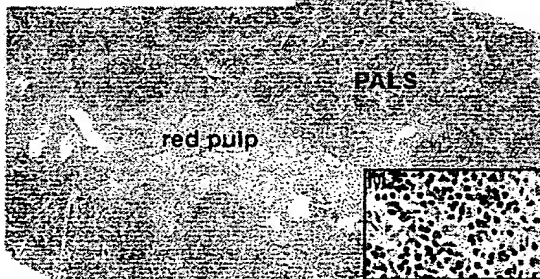


FIG. 10F

Spleen-WX11#6

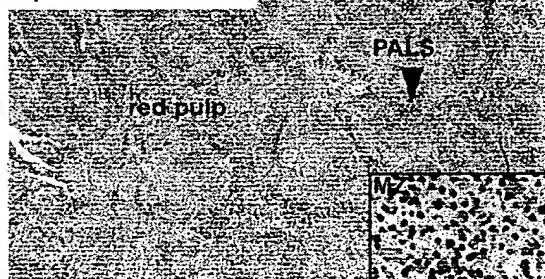


FIG. 10G

Ileum-control#25

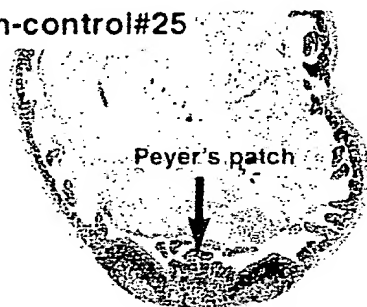


FIG. 10H

Ileum-WX11#32

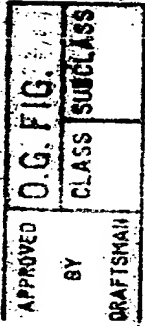
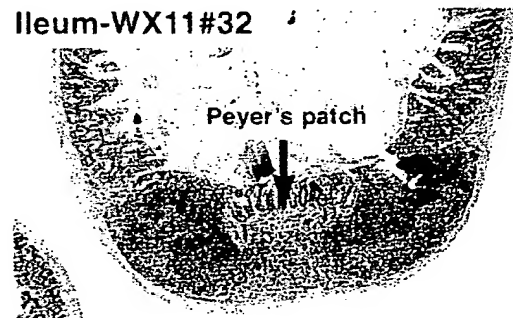




FIG. 11A



Control#5-H&E

FIG. 11B

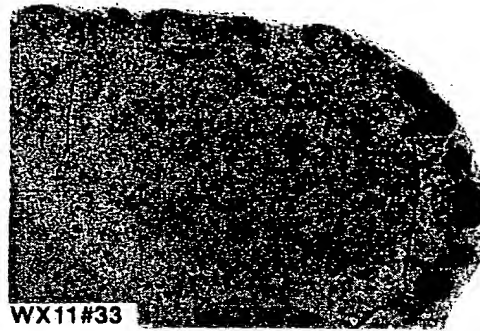
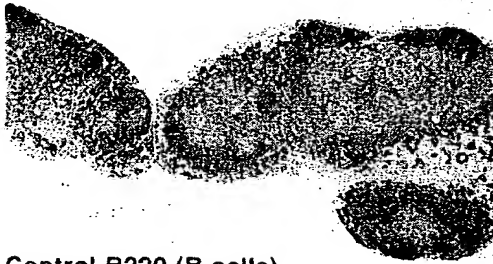


FIG. 11C



Control-B220 (B cells)

FIG. 11D

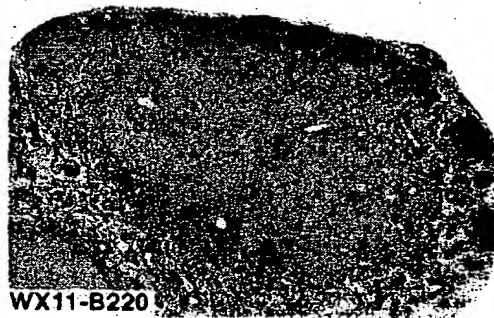
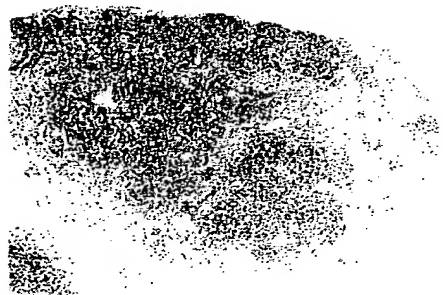


FIG. 11E



Control-CD3 (T cells)

FIG. 11F



WX11-CD3

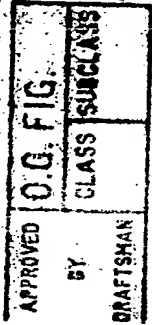




FIGURE 12A.1

GCTGGTACGCCTGCAGGTACCGGTCCGGAATTCCCGGGTCGACCCACGCGTCCGCCCACGCG -138
TCCGCGGGAGCGCAGTTAGAGCCGATCTCCCGCGCCCCGAGGTTGCTCCTCTCCGAGGTCTC -76
CCGCGGCCCCAAGTTCTCCGCGCCCCGAGGTCTCCGCGCCCCGAGGTCTCCGCGCCCCGAGGT -14
CTCCGCCCCGACC -1

ATG CGG CTG GGC AGT CCT GGA CTG CTC TTC CTG CTC TTC AGC AGC 45
M R L G S P G L L F L L F S S
5 10 15

CTT CGA GCT GAT ACT CAG GAG AAG GAA GTC AGA GCG ATG GTA GGC 90
L R A *D *T *Q *E K *E V R A *M V G
20 25 30

AGC GAC GTG GAG CTC AGC TGC GCT TGC CCT GAA GGA AGC CGT TTT 135
S D V E L S C A C P E G S R F
35 40 45

GAT TTA AAT GAT GTT TAC GTA TAT TGG CAA ACC AGT GAG TCG AAA 180
D L N D V Y V Y W Q T S E S K
50 55 60

ACC GTG GTG ACC TAC CAC ATC CCA CAG AAC AGC TCC TTG GAA AAC 225
T V V T Y H I P Q N S S L E N
65 70 75

GTG GAC AGC CGC TAC CGG AAC CGA GCC CTG ATG TCA CCG GCC GGC 270
V D S R Y R N R A L M S P A G
80 85 90

ATG CTG CGG GGC GAC TTC TCC CTG CGC TTG TTC AAC GTC ACC CCC 315
M L R G D F S L R L F N V T P
95 100 105

CAG GAC GAG CAG AAG TTT CAC TGC CTG GTG TTG AGC CAA TCC CTG 360
Q D E Q K F H C L V L S Q S L
110 115 120

GGA TTC CAG GAG GTT TTG AGC GTT GAG GTT ACA CTG CAT GTG GCA 405
G F Q E V L S V E V T L H V A
125 130 135

GCA AAC TTC AGC GTG CCC GTC GTC AGC GCC CCC CAC AGC CCC TCC 450
A N F S V P V V S A P H S P S
140 145 150

CAG GAT GAG CTC ACC TTC ACG TGT ACA TCC ATA AAC GGC TAC CCC 495
Q D E L T F T C T S I N G Y P
155 160 165

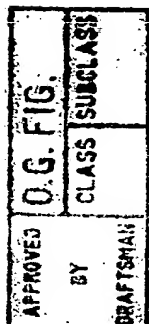
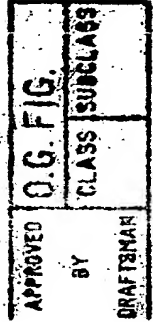




FIGURE 12A.2



AGG CCC AAC GTG TAC TGG ATC AAT AAG ACG GAC AAC AGC CTG CTG 540
R P N V Y W I N K T D N S L L
170 175 180

GAC CAG GCT CTG CAG AAT GAC ACC GTC TTC TTG AAC ATG CGG GGC 585
D Q A L Q N D T V F L N M R G
185 190 195

TTG TAT GAC GTG GTC AGC GTG CTG AGG ATC GCA CGG ACC CCC AGC 630
L Y D V V S V L R I A R T P S
200 205 210

GTG AAC ATT GGC TGC TGC ATA GAG AAC GTG CTT CTG CAG CAG AAC 675
V N I G C C I E N V L L Q Q N
215 220 225

CTG ACT GTC GGC AGC CAG ACA GGA AAT GAC ATC GGA GAG AGA GAC 720
L T V G S Q T G N D I G E R D
230 235 240

AAG ATC ACA GAG AAT CCA GTC AGT ACC GGC GAG AAA AAC GCG GCC 765
K I T E N P V S T G E K N A A
245 250 255

ACG TGG AGC ATC CTG GCT GTC CTG TGC CTG CTT GTG GTC GTG GCG 810
T W S I L A V L C L L V V V A
260 265 270

GTG GCC ATA GGC TGG GTG TGC AGG GAC CGA TGC CTC CAA CAC AGC 855
V A I G W V C R D R C L Q H S
275 280 285

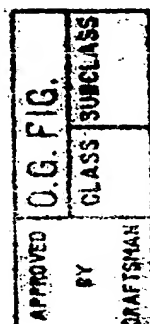
TAT GCA GGT GCC TGG GCT GTG AGT CCG GAG ACA GAG CTC ACT GGC 900
Y A G A W A V S P E T E L T G
300

CAC GTT TGA 909
H V STOP
302

CCGGAGCTCACC GCCCAGAGCGTGGACAGGGCTTCCGTGAGACGCCACCGTGAGAGGCCAGG 971
TGGCAGCTTGAGCATGGACTCCCAGACTGCAGGGGAGCACTTGGGGCAGCCCCAGAAGGAC 1033
CACTGCTGGATCCCAGGGGAGAACCTGCTGGCGTTGGCTGTGATCCTGGAATGAGGCCCTTTC 1095



FIGURE 12B



human	MRLGSP----	-----G	L-LF-LLFSS	LRADTQEKEV	25	
mouse	MQLKPCPFVS	LGTRQPVWKK	LHVSSGFFSG	LGLFLLLLSS	LCAASAETEV	50
Consensus	M.L..P....G	L.LF.LL.SS	L.A...E.EV	50	
human	RAMVGSDEL	SCACPEGSRF	DLNDVYVYWQ	TSESKTVVTY	HIPQNSSLN	75
mouse	GAMVGSNVVL	SCIDPHRRHF	NLSGLYVYWQ	IENPEVSVTY	YLPYKSPGIN	100
Consensus	.AMVGS.V.L	SC..P....F	.L...YVYWQVTY	..P..S...N	100
human	VDSRYNRAL	MSPAGMLRGD	FSLRLFNVTP	QDEQKFHCLV	LSQ-SLGFQE	124
mouse	VDSSYKNRGH	LSLDSMKQGN	FSLYLKNVTP	QDTQEFTCRV	FMNTATELVK	150
Consensus	VDS.Y.NR..	.S...M..G.	FSL.L.NVTP	QD.Q.F.C.V	150
human	VLSVEVTLHV	AANFSVPVVS	APHSPSQ-DE	LTFTCTSING	YPRPNVYWIN	173
mouse	ILEEVVRLRV	AANFSTPVIS	TSDSSNPGQE	RTYTCMSKNG	YPEPNLYWIN	200
Consensus	.L...V.L.V	AANFS.PV.S	...S.....E	.T.TC.S.NG	YP.PN.YWIN	200
human	KTDNSLLDQA	LQNDTVFLNM	RGLYDVVSVL	RIARTPSVNI	GCCIENVLLQ	223
mouse	TTDNSLIDTA	LQNNTVYLNK	LGLYDVISTL	RLPWTSRGDV	LCCVENVALH	250
Consensus	.TDNSL.D.A	LQN.TV.LN.	.GLYDV.S.L	R...T.....	.CC.ENV.L.	250
human	QNLTVGSQTG	NDIGERDKIT	ENPVSTGEKN	AATWSILAVL	CLLVVVAVAI	273
mouse	QNITSISQAE	SFTGNNTKNP	QETHNNELKV	LV--PVLAVL	AAAFVSFII	298
Consensus	QN.T..SQ..	...G...K..K.LAVLV...I	300
human	GWVCRDRCLQ	HSYAGAWAVS	PETELTGHV			302
mouse	YR--RTR-PH	RSYTGPKTVQ	LE--LTDHA			322
ConsensusR.R...	.SY.G...V.	.E..LT.H.			329

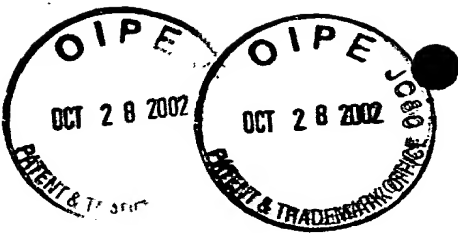


FIGURE 13A.1

APPROVED	BY	DRAFTSMAN	O.G. FIG.
			CLASS SUBCLASS

AACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAGCTCTAATACGA	-111
CTCACTATAGGGAAAGCTGGTACGCCTGCAGGTACCGGTCCGGAATCCCGGGTC	-56
GACCCACGCGTCCGTGAACACTGAACGCGAGGACTGTAACTGTTTCTGGCAAAC	-1
ATG AAG TCA GGC CTC TGG TAT TTC TTT CTC TTC TGC TTG CGC ATT	45
M K S G L W Y F F L F C L R I	
5 10 15	
AAA GTT TTA ACA GGA GAA ATC AAT GGT TCT GCC AAT TAT GAG ATG	90
K V L T *G *E I N G S A N Y E M	
20 25 30	
TTT ATA TTT CAC AAC GGA GGT GTA CAA ATT TTA TGC AAA TAT CCT	135
F I F H N G G V Q I L C K Y P	
35 40 45	
GAC ATT GTC CAG CAA TTT AAA ATG CAG TTG CTG AAA GGG GGG CAA	180
D I V Q Q F K M Q L L K G G Q	
50 55 60	
ATA CTC TGC GAT CTC ACT AAG ACA AAA GGA AGT GGA AAC ACA GTG	225
I L C D L T K T K G S G N T V	
65 70 75	
TCC ATT AAG AGT CTG AAA TTC TGC CAT TCT CAG TTA TCC AAC AAC	270
S I K S L K F C H S Q L S N N	
80 85 90	
AGT GTC TCT TTT TTT CTA TAC AAC TTG GAC CAT TCT CAT GCC AAC	315
S V S F F L Y N L D H S H A N	
95 100 105	
TAT TAC TTC TGC AAC CTA TCA ATT TTT GAT CCT CCT CCT TTT AAA	360
Y Y F C N L S I F D P P P F K	
110 115 120	
GTA ACT CTT ACA GGA GGA TAT TTG CAT ATT TAT GAA TCA CAA CTT	405
V T L T G G Y L H I Y E S Q L	
125 130 135	
TGT TGC CAG CTG AAG TTC TGG TTA CCC ATA GGA TGT GCA GCC TTT	450
C C Q L K F W L P I G C A A F	
140 145 150	
GTT GTA GTC TGC ATT TTG GGA TGC ATA CTT ATT TGT TGG CTT ACA	495
V V V C I L G C I L I C W L T	
155 160 165	



FIGURE 13A.2

APPROVED	BY	DRAFTSMAN	O.G. FIG.	CLASS	SUBCLASS

AAA AAG AAG TAT TCA TCC AGT GTG CAC GAC CCT AAC GGT GAA TAC 540
K K K Y S S S V H D P N G E Y
170 175 180

ATG TTC ATG AGA GCA GTG AAC ACA GCC AAA AAA TCT AGA CTC ACA 585
M F M R A V N T A K K S R L T
185 190 195

GAT GTG ACC CTA TAA 600
D V T L STOP
199

TATGGAACCTCTGGCACCCAGGCATGAAGCACGTTGGCCAGTTTTCTCAACTTGA 655
AGTGCAAGATTCTCTTATTTCCGGGACCACGGAGAGTCTGACTTAACTACATACA 710
TCTTCTGCTGGTGTTTTGTTCAATCTGGAAGAATGACTGTATCAGTCAATGGGGA 765
TTTTAACAGACTGCCTTGGTACTGCCGAGTCCTCTCAAAACAAACACCCCTCTTGC 820
AACCAGCTTTGGAGAAAGCCCAGCTCCTGTGTGCTCACTGGGAGTGGAATCCCTG 875
TCTCCACATCTGCTCCTAGCAGTGCATCAGCCAGTAAAAACAAACACATTTACAAG 930
AAAAATGTTTTAAAGATGCCAGGGGTACTGAATCTGCAAAGCAAATGAGCAGCCA 985
AGGACCAGCATCTGTCCGCATTTCACTATCATACTACCTCTTCTTTCTGTAGGGA 1040
TGAGAATTCTCTTTTAATCAGTCAAGGGAGATGCTTCAAAGCTGGAGCTATTTT 1095
ATTTCTGAGATGTTGATGTGAACTGTACATTAGTACATACTCAGTACTCTCCTTC 1150
AATTGCTGAACCCAGTTGACCATTTTACCAAGACTTTAGATGCTTTCTTGTGCC 1205



FIGURE 13B

APPROVED	O.G. FIG.	
	CLASS	SUBCLASS
BY	DRAFTSMAN	

hCRP1	MKSGWLWYFFLFCLRIKVLGTGEINGSANYEMFIFHNGGVQILCKYPDIVQQ	50
mCRP1	. . : . .: :	50
hCRP1	MKPYFCRVFVFCFLIRLLTGEINGSADHRMFSFHNGGVQISCKYPETVQQ	50
hCRP1	FKMQLLKGGQILCDLTCTKGSGNTVSIKSLKFCHSQLSNNSVSFFLYNLD	100
mCRP1	. : : .	100
hCRP1	LKMRLFREREVLCELCTKGSGNAVSIKNPMLCLYHLSNNSVSFFLNNPD	100
hCRP1	HSHANYFFCNLSIFDPPPFKV.TLTGGYLHIYESQLCCQLKFWLPIGCAA	149
mCRP1	. . . :	150
hCRP1	SSQGSYYFCSLSIFDPPPFQERNLSGGYLHIYESQLCCQLKLWLPVGCAA	150
hCRP1	FVVVCILGCILICWLTKKKYSSSVHDPNGEYMFMRVNTAKKSRLTDVTL	199
mCRP1	: .	200
	FVVVLLFGCILIIFWSKKKYGSSVHDPNSEYMFMAAVNTNKKSLAGVTS	200



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAETSMAN		

FIG. 14A

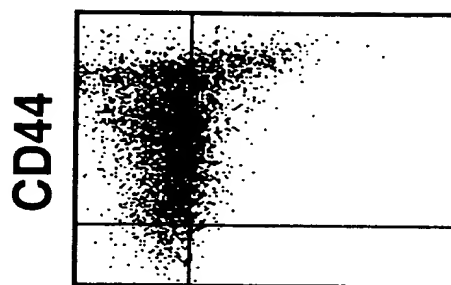
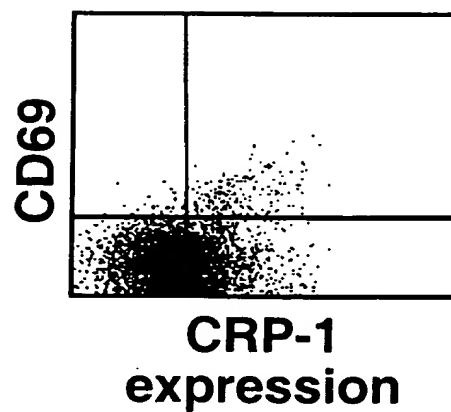


FIG. 14B



FIG. 14C





APPROVED	0.G. FIG.
BY	CLASS
DRAFTSMAN	SUBCLASS

FIG. 15A

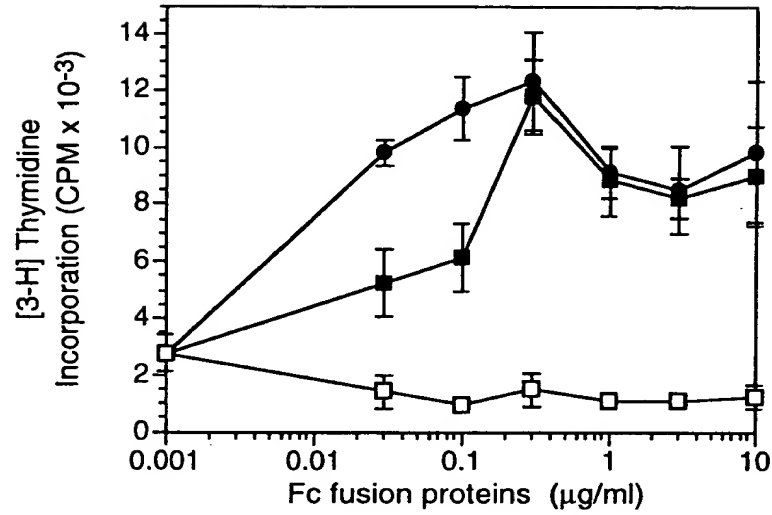
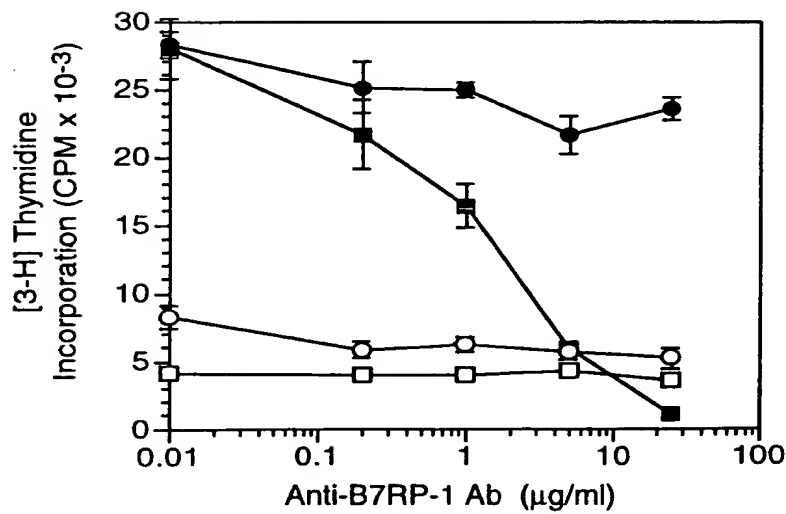


FIG. 15B





O.G. FIG.	
APPROVED	BY CLASS SUBCLASS
DRAFTSMAN	

FIG. 16A

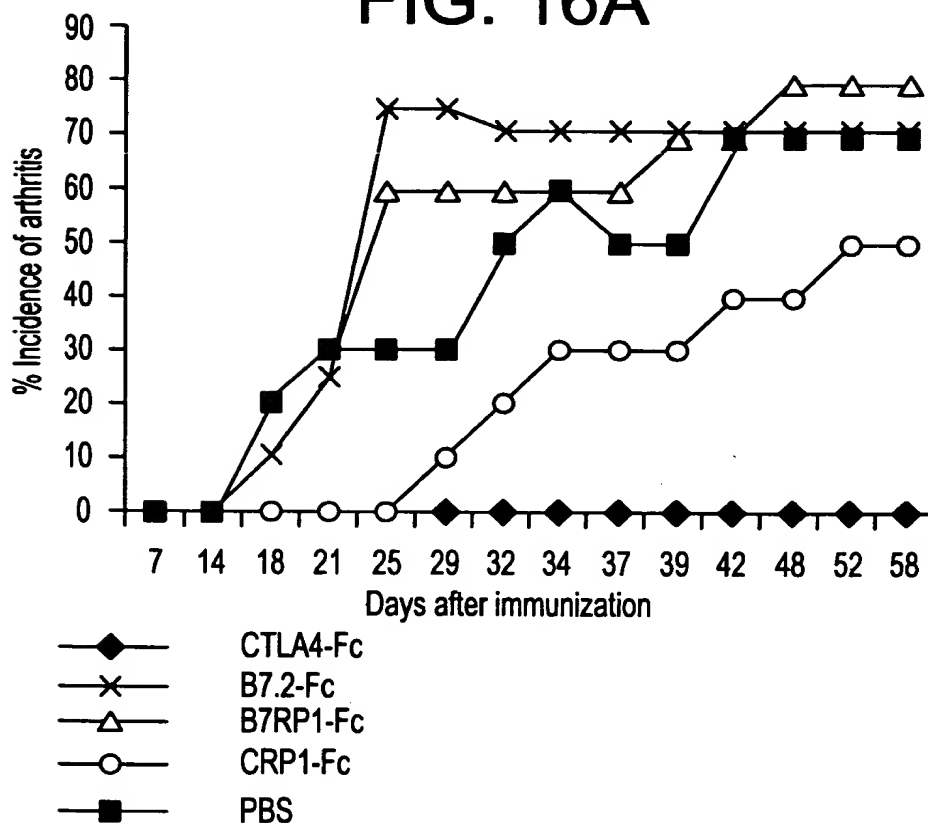


FIG. 16B

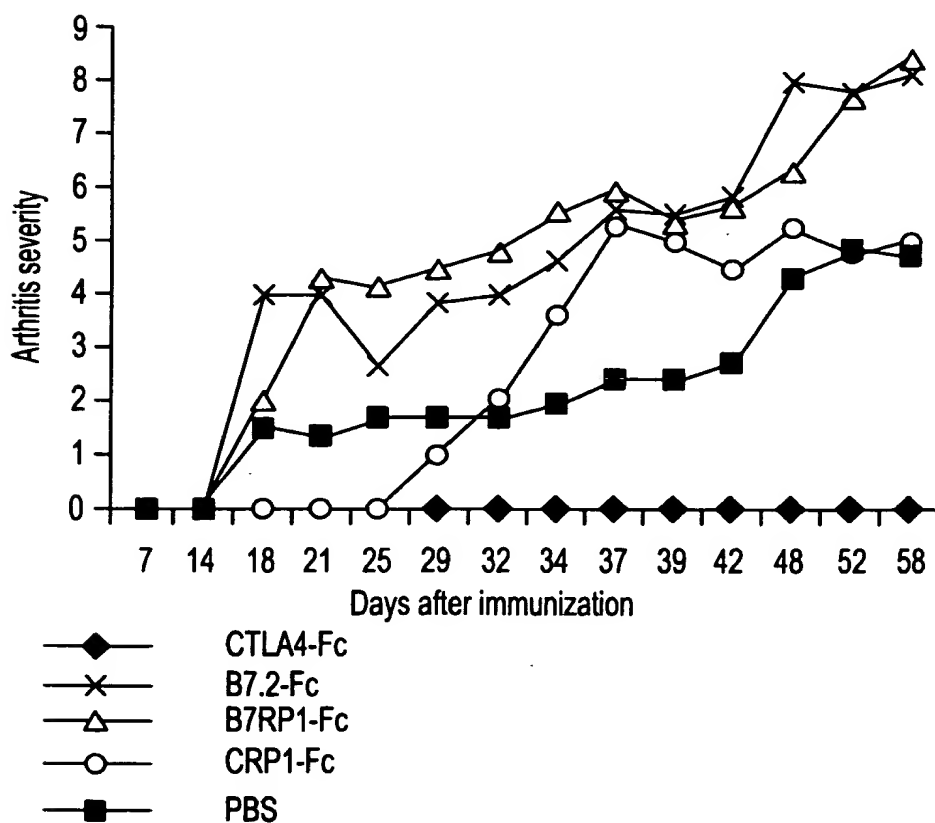
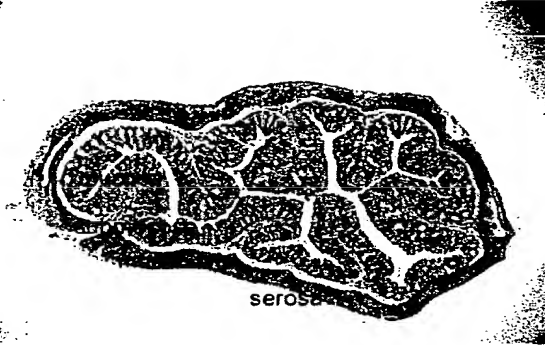


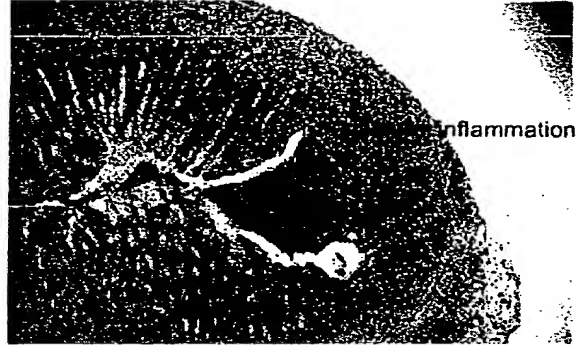


FIG. 17A



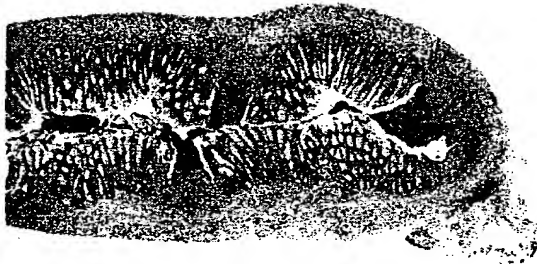
Control mouse#53F: Prox. colon 40X

FIG. 17B



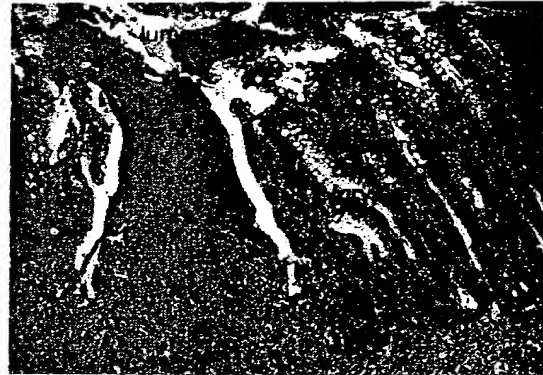
Mouse#111F: Prox. colon 40X

FIG. 17C



Mouse#111F: Prox. colon 20X

FIG. 17D



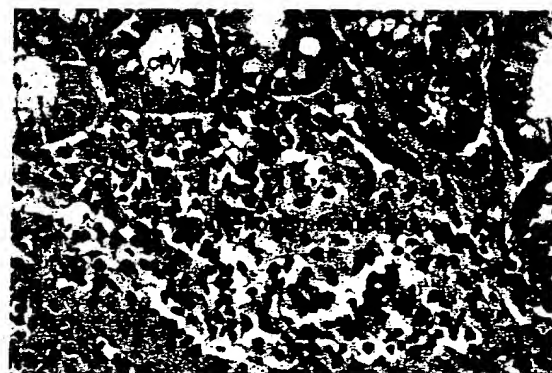
Mouse#111F: closeup of mucosa 100X

FIG. 17E



Mouse#112F: Giant cell, submucosa

FIG. 17F



Mouse#112F: epithelioid macrophages

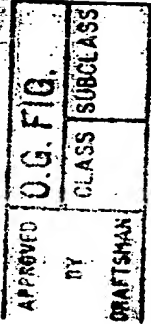




FIG. 18A



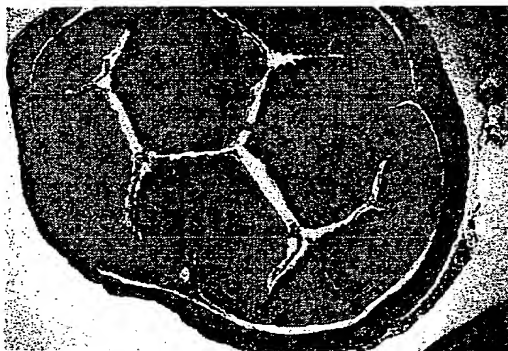
Control mouse#53F: Distal colon, 40X

FIG. 18B



Mouse#111F: Distal colitis, 40X

FIG. 18C



Mouse#55M: Distal colitis, 40X

FIG. 18D



Mouse#112F: Distal colon, 40X

FIG. 18E

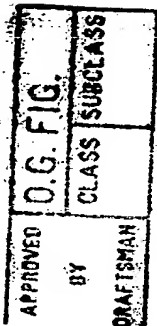


Mouse#112: CD3+ T-cells, 40X

FIG. 18F



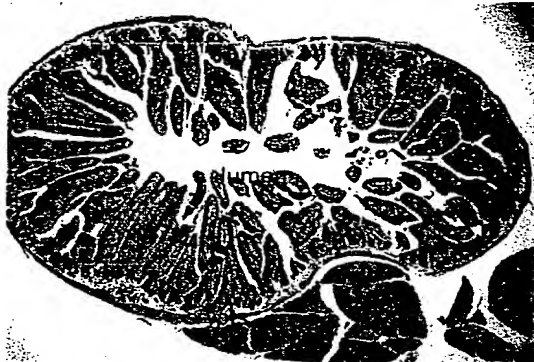
Mouse#112: closeup, 100X





APPROVED	O.G. FIG.	
	BY	CLASS
	SUBCLASS	
DRAFTSMAN		

FIG. 19A



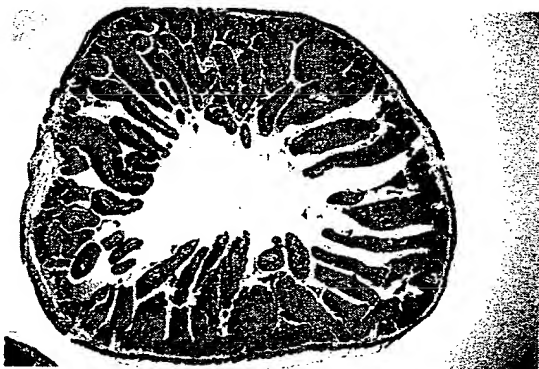
Control mouse#53F: duodenum, 40X

FIG. 19B



Mouse#51F: duodenum, 40X

FIG. 19C



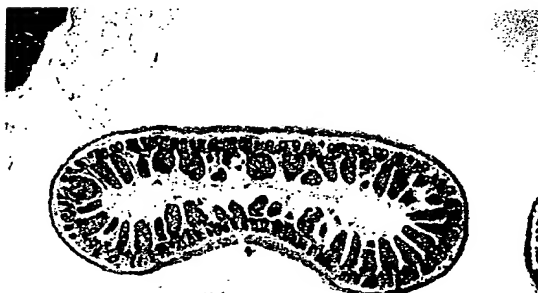
Control mouse#53F: jejunum, 40X

FIG. 19D



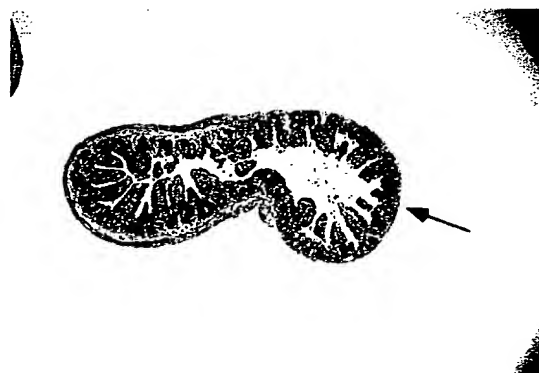
Mouse#51F: jejunal hyperplasia, 40X

FIG. 19E



Mouse#53F: ileum, 40X

FIG. 19F



Mouse#231M: ileal atrophy, 40X



APPROVED	BY	DRAFTSMAN
O.G. FIG.	CLASS	SUBCLASS

FIG. 20

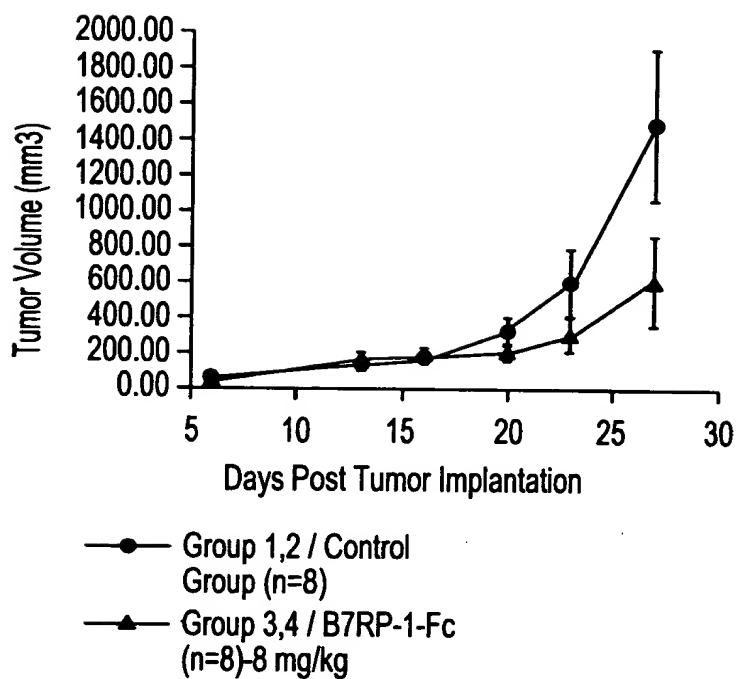




FIG. 21A

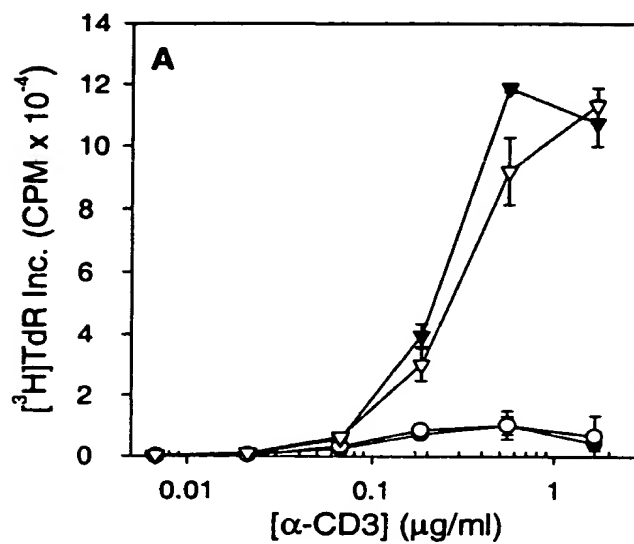


FIG. 21B

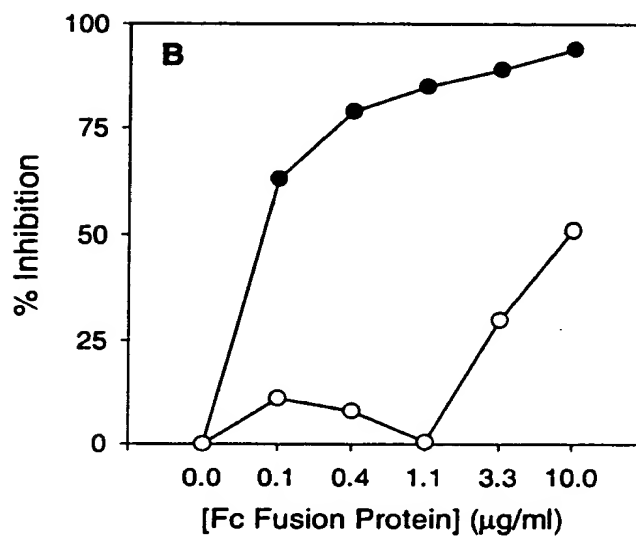
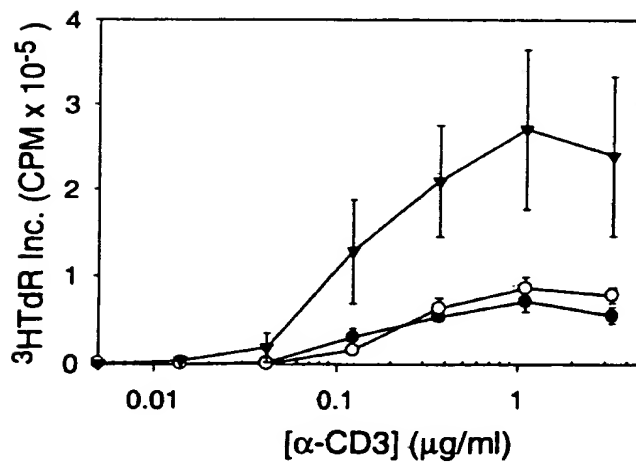


FIG. 21C





APPROVED	BY	DRAFTSMAN
O.G. FIG.		CLASS SUBCLASS

FIG. 21D

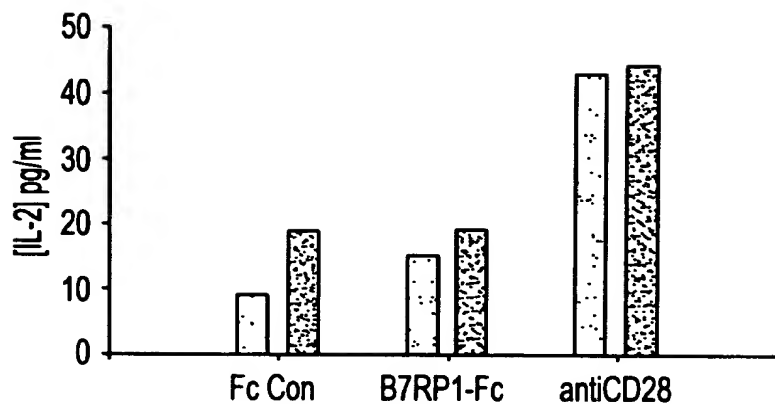


FIG. 21E

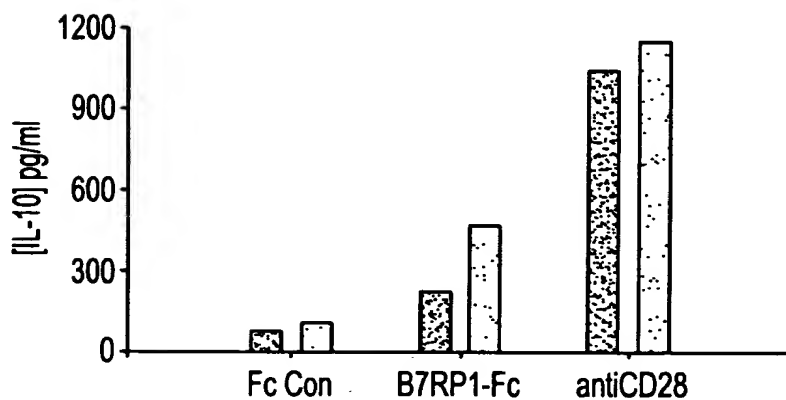
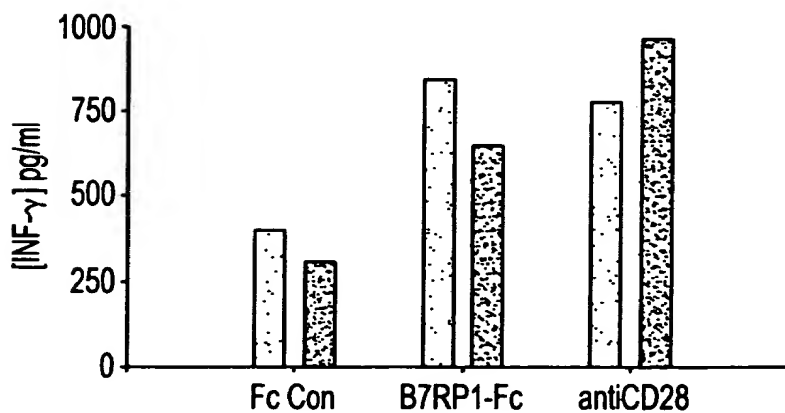


FIG. 21F





APPROVED	BY	DRAFTSMAN
O.G. FIG.		CLASS SUBCLASS

FIG. 22

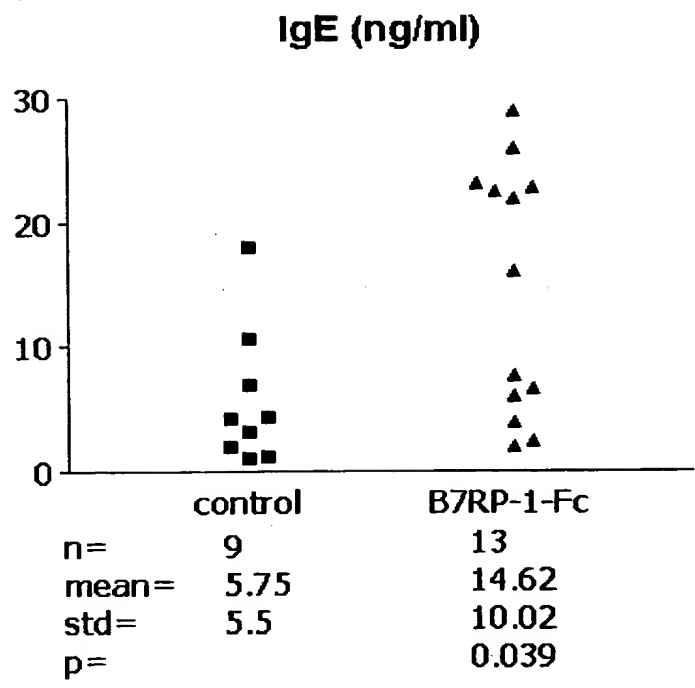




FIG. 23

